

## SEQUENCE LISTING

&lt;151&gt; 1999-06-01

&lt;160&gt; 17

5

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 409

10

&lt;212&gt; PRT

&lt;213&gt; Salmonella typhimurium

&lt;400&gt; 1

Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn Asn  
15 1 5 10 15His Ser Val Glu Asn Ser Ser Gln Thr Ala Ser Gln Ser Val Ser Ala  
20 20 25 30Lys Asp Ile Leu Asn Ser Ile Gly Ile Ser Ser Ser Lys Val Ser Asp  
25 35 40 45Leu Gly Leu Ser Pro Thr Leu Ser Ala Pro Ala Pro Gly Val Leu Thr  
25 50 55 60Gln Thr Pro Gly Thr Ile Thr Ser Ser Leu Lys Ala Ser Ile Gln Asn  
65 70 75 80Thr Asp Met Asn Gln Asp Leu Asn Ala Leu Ala Asn Asn Val Thr Thr  
30 85 90 95Lys Ala Asn Glu Val Val Gln Thr Gln Leu Arg Glu Gln Gln Ala Glu  
100 105 110Val Gly Lys Phe Phe Asp Ile Ser Gly Met Ser Ser Ser Ala Val Ala  
35 115 120 125Leu Leu Ala Ala Ala Asn Thr Leu Met Leu Thr Leu Asn Gln Ala Asp  
40 130 135 140Ser Lys Leu Ser Gly Lys Leu Ser Leu Val Ser Phe Asp Ala Ala Lys  
145 150 155 160

Thr Thr Ala Ser Ser Met Met Arg Glu Gly Met Asn Ala Leu Ser Gly  
165 170 175

5 Ser Ile Ser Gln Ser Ala Leu Gln Leu Gly Ile Thr Gly Val Gly Ala  
180 185 190

Lys Leu Glu Tyr Lys Gly Leu Gln Asn Glu Arg Gly Ala Leu Lys His  
195 200 205

10 Asn Ala Ala Lys Ile Asp Lys Leu Thr Thr Glu Ser His Ser Ile Lys  
210 215 220

Asn Val Leu Asn Gly Gln Asn Ser Val Lys Leu Gly Ala Glu Gly Val  
225 230 235 240

15 Asp Ser Leu Lys Ser Leu Asn Ile Arg Lys Pro Val Pro Met Arg Arg  
245 250 255

Lys Ile Leu Met Met Arg Arg Leu Asn Leu Met Pro Glu Pro Ala Pro  
20 260 265 270

Arg Lys Val Trp Val Leu Lys Thr Val Ile Asn Lys Val Ser Leu Asn  
275 280 285

25 Ile Tyr Ile Leu Ser Lys Arg Leu Glu Ser Val Glu Ser Asp Ile Arg  
290 295 300

Leu Glu Gln Asn Tyr Met Asp Ile Thr Arg Ile Asp Ser Ala Gln Asp  
305 310 315 320

30 Ala Asp Asp Gly Arg Ser Asp Tyr Glu Glu Leu Gly His Gly Arg Trp  
325 330 335

Tyr Cys Arg Gly Val Arg Ala Val Arg Arg Tyr Ser Gly Asn Val Ser  
35 340 345 350

Glu Gln Gln Ile Ser Gln Val Asn Asn Arg Val Ala Ser Thr Ala Ser  
355 360 365

40 Asp Glu Ala Arg Glu Ser Ser Arg Lys Ser Thr Ser Leu Ile Gln Glu  
370 375 380

Met Leu Lys Thr Met Glu Ser Ile Asn Gln Ser Lys Ala Ser Ala Leu  
385 390 395 400

45

Ala Ala Ile Ala Gly Asn Ile Arg Ala  
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5     <210> 2  
      <211> 382  
      <212> PRT  
      <213> *Shigella flexneri*

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15    Glu Asn Val Met Glu Ile Gln Asn Thr Lys Pro Thr Gln Thr Leu Tyr  
          20           25           30

      Thr Asp Ile Ser Thr Lys Gln Thr Gln Ser Ser Ser Glu Thr Gln Lys  
          35           40           45

20    Ser Gln Asn Tyr Gln Gln Ile Ala Ala His Ile Pro Leu Asn Val Gly  
          50           55           60

      Lys Asn Pro Val Leu Thr Thr Thr Leu Asn Asp Asp Gln Leu Leu Lys  
          65           70           75           80

25    Leu Ser Glu Gln Val Gln His Asp Ser Glu Ile Ile Ala Arg Leu Thr  
          85           90           95

30    Asp Lys Lys Met Lys Asp Leu Ser Glu Met Ser His Thr Leu Thr Pro  
          100           105           110

      Glu Asn Thr Leu Asp Ile Ser Ser Leu Ser Ser Asn Ala Val Ser Leu  
          115           120           125

35    Ile Ile Ser Val Ala Val Leu Leu Ser Ala Leu Arg Thr Ala Glu Thr  
          130           135           140

      Lys Leu Gly Ser Gln Leu Ser Leu Ile Ala Phe Asp Ala Thr Lys Ser  
          145           150           155           160

40    Ala Ala Glu Asn Ile Val Arg Gln Gly Leu Ala Ala Leu Ser Ser Ser  
          165           170           175

45    Ile Thr Gly Ala Val Thr Gln Val Gly Ile Thr Gly Ile Gly Ala Lys  
          180           185           190

Lys Thr His Ser Gly Ile Ser Asp Gln Lys Gly Ala Leu Arg Lys Asn  
195 200 205

5 Leu Ala Thr Ala Gln Ser Leu Glu Lys Glu Leu Ala Gly Ser Lys Leu  
210 215 220

Gly Leu Asn Lys Gln Ile Asp Thr Asn Ile Thr Ser Pro Gln Thr Asn  
225 230 235 240

10 Ser Ser Thr Lys Phe Leu Gly Lys Asn Lys Leu Ala Pro Asp Asn Ile  
245 250 255

Ser Leu Ser Thr Glu His Lys Thr Ser Leu Ser Ser Pro Asp Ile Ser  
260 265 270

15 Leu Gln Asp Lys Ile Asp Thr Gln Arg Arg Thr Tyr Glu Leu Asn Thr  
275 280 285

20 Leu Ser Ala Gln Gln Lys Gln Asn Ile Gly Arg Ala Thr Met Glu Thr  
290 295 300

Ser Ala Val Ala Gly Asn Ile Ser Thr Ser Gly Gly Arg Tyr Ala Ser  
305 310 315 320

25 Ala Leu Glu Glu Glu Glu Gln Leu Ile Ser Gln Ala Ser Ser Lys Gln  
325 330 335

Ala Glu Glu Ala Ser Gln Val Ser Lys Glu Ala Ser Gln Ala Thr Asn  
340 345 350

30 Gln Leu Ile Gln Lys Leu Leu Asn Ile Ile Asp Ser Ile Asn Gln Ser  
355 360 365

35 Lys Asn Ser Ala Ala Ser Gln Ile Ala Gly Asn Ile Arg Ala  
370 375 380

<210> 3  
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40 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NdeI  
45 restriction site

<400> 3  
gaga 4

5 <210> 4  
<211> 29  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 4  
gagacatatg ttatcagagc aggttcagc 29

15 <210> 5  
<211> 30  
<212> DNA  
<213> Artificial Sequence

20 <220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 5  
gagaggatcc ttaagctcga atgttaccag 30

25 <210> 6  
<211> 27  
<212> DNA  
<213> Artificial Sequence

30 <220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 6  
35 gagacatatg ttgcaaaagc aatttgc 27

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40 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

45 <400> 7  
gagaggatcc ttaggtgtca attttatcct gc 32

<210> 8  
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5 <213> Artificial Sequence

<220>  
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10 <400> 8  
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<210> 9  
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15 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

20 <400> 9  
gagaggatcc ttaggtgtca attttatcct gc 32

<210> 10  
25 <211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
30 <223> Description of Artificial Sequence: PCR Primer

<400> 10  
gagacatatg ttgcaaaagc aa 22

35 <210> 11  
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<213> Artificial Sequence

40 <220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 11  
gagactcgag atgcgtttt ttggcaccg 29

45 <210> 12

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<213> Artificial Sequence

5 <220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 12  
gagactcgag acccagagaa gaacttacg 29

10 <210> 13  
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15 <220>  
<223> Description of Artificial Sequence: PCR Primer

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20 gagaggatcc ttaagctga atgtaccag 30

<210> 14  
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25 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

30 <400> 14  
gagacatatg ttgcaaaagc aatttgc 27

<210> 15  
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35 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

40 <400> 15  
gagactcgag taactttaaa agttgatcat c 31

<210> 16  
45 <211> 28  
<212> DNA

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<223> Description of Artificial Sequence: PCR Primer

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<400> 16

gagactcgag ctgcccactg ctcaatct

28

<210> 17

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

15

<223> Description of Artificial Sequence: PCR Primer

<400> 17

gagaggatcc ttaagctcga atgttaccag

30

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## SEQUENCE LISTING

<110> University of Kansas Center for Research  
Walter Reed Army Institute for Research

<120> METHODS FOR THE PRODUCTION OF PURIFIED INVASIN PROTEIN AND USE THEREOF

<130> UOK 5320.1

<150> PCT/US99/24931

<151> 1999-10-21

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 409

<212> PRT

<213> Salmonella typhimurium

<400> 1

Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn Asn  
1 5 10 15

His Ser Val Glu Asn Ser Ser Gln Thr Ala Ser Gln Ser Val Ser Ala  
20 25 30

Lys Asp Ile Leu Asn Ser Ile Gly Ile Ser Ser Ser Lys Val Ser Asp  
35 40 45

Leu Gly Leu Ser Pro Thr Leu Ser Ala Pro Ala Pro Gly Val Leu Thr  
50 55 60

Gln Thr Pro Gly Thr Ile Thr Ser Ser Leu Lys Ala Ser Ile Gln Asn  
65 70 75 80

Thr Asp Met Asn Gln Asp Leu Asn Ala Leu Ala Asn Asn Val Thr Thr  
85 90 95

Lys Ala Asn Glu Val Val Gln Thr Gln Leu Arg Glu Gln Gln Ala Glu  
100 105 110

Val Gly Lys Phe Phe Asp Ile Ser Gly Met Ser Ser Ser Ala Val Ala  
115 120 125

Leu Leu Ala Ala Ala Asn Thr Leu Met Leu Thr Leu Asn Gln Ala Asp  
130 135 140

Ser Lys Leu Ser Gly Lys Leu Ser Leu Val Ser Phe Asp Ala Ala Lys  
145 150 155 160

Thr Thr Ala Ser Ser Met Met Arg Glu Gly Met Asn Ala Leu Ser Gly  
165 170 175

Ser Ile Ser Gln Ser Ala Leu Gln Leu Gly Ile Thr Gly Val Gly Ala

180

185

190

Lys Leu Glu Tyr Lys Gly Leu Gln Asn Glu Arg Gly Ala Leu Lys His  
195 200 205

Asn Ala Ala Lys Ile Asp Lys Leu Thr Thr Glu Ser His Ser Ile Lys  
210 215 220

Asn Val Leu Asn Gly Gln Asn Ser Val Lys Leu Gly Ala Glu Gly Val  
225 230 235 240

Asp Ser Leu Lys Ser Leu Asn Ile Arg Lys Pro Val Pro Met Arg Arg  
245 250 255

Lys Ile Leu Met Met Arg Arg Leu Asn Leu Met Pro Glu Pro Ala Pro  
260 265 270

Arg Lys Val Trp Val Leu Lys Thr Val Ile Asn Lys Val Ser Leu Asn  
275 280 285

Ile Tyr Ile Leu Ser Lys Arg Leu Glu Ser Val Glu Ser Asp Ile Arg  
290 295 300

Leu Glu Gln Asn Tyr Met Asp Ile Thr Arg Ile Asp Ser Ala Gln Asp  
305 310 315 320

Ala Asp Asp Gly Arg Ser Asp Tyr Glu Glu Leu Gly His Gly Arg Trp  
325 330 335

Tyr Cys Arg Gly Val Arg Ala Val Arg Arg Tyr Ser Gly Asn Val Ser  
340 345 350

Glu Gln Gln Ile Ser Gln Val Asn Asn Arg Val Ala Ser Thr Ala Ser  
355 360 365

Asp Glu Ala Arg Glu Ser Ser Arg Lys Ser Thr Ser Leu Ile Gln Glu  
370 375 380

Met Leu Lys Thr Met Glu Ser Ile Asn Gln Ser Lys Ala Ser Ala Leu  
385 390 395 400

Ala Ala Ile Ala Gly Asn Ile Arg Ala  
405

<210> 2

<211> 382

<212> PRT

<213> *Shigella flexneri*

<400> 2

Met Leu Gln Lys Gln Phe Cys Asn Lys Leu Leu Leu Asp Thr Asn Lys  
1 5 10 15

Glu Asn Val Met Glu Ile Gln Asn Thr Lys Pro Thr Gln Thr Leu Tyr  
20 25 30

Thr	Asp	Ile	Ser	Thr	Lys	Gln	Thr	Gln	Ser	Ser	Ser	Glu	Thr	Gln	Lys	35	40	45	
Ser	Gln	Asn	Tyr	Gln	Gln	Ile	Ala	Ala	His	Ile	Pro	Leu	Asn	Val	Gly	50	55	60	
Lys	Asn	Pro	Val	Leu	Thr	Thr	Thr	Leu	Asn	Asp	Asp	Gln	Leu	Leu	Lys	65	70	75	80
Leu	Ser	Glu	Gln	Val	Gln	His	Asp	Ser	Glu	Ile	Ile	Ala	Arg	Leu	Thr	85	90	95	
Asp	Lys	Lys	Met	Lys	Asp	Leu	Ser	Glu	Met	Ser	His	Thr	Leu	Thr	Pro	100	105	110	
Glu	Asn	Thr	Leu	Asp	Ile	Ser	Ser	Leu	Ser	Ser	Asn	Ala	Val	Ser	Leu	115	120	125	
Ile	Ile	Ser	Val	Ala	Val	Leu	Leu	Ser	Ala	Leu	Arg	Thr	Ala	Glu	Thr	130	135	140	
Lys	Leu	Gly	Ser	Gln	Leu	Ser	Leu	Ile	Ala	Phe	Asp	Ala	Thr	Lys	Ser	145	150	155	160
Ala	Ala	Glu	Asn	Ile	Val	Arg	Gln	Gly	Leu	Ala	Ala	Leu	Ser	Ser	Ser	165	170	175	
Ile	Thr	Gly	Ala	Val	Thr	Gln	Val	Gly	Ile	Thr	Gly	Ile	Gly	Ala	Lys	180	185	190	
Lys	Thr	His	Ser	Gly	Ile	Ser	Asp	Gln	Lys	Gly	Ala	Leu	Arg	Lys	Asn	195	200	205	
Leu	Ala	Thr	Ala	Gln	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Gly	Ser	Lys	Leu	210	215	220	
Gly	Leu	Asn	Lys	Gln	Ile	Asp	Thr	Asn	Ile	Thr	Ser	Pro	Gln	Thr	Asn	225	230	235	240
Ser	Ser	Thr	Lys	Phe	Leu	Gly	Lys	Asn	Lys	Leu	Ala	Pro	Asp	Asn	Ile	245	250	255	
Ser	Leu	Ser	Thr	Glu	His	Lys	Thr	Ser	Leu	Ser	Ser	Pro	Asp	Ile	Ser	260	265	270	
Leu	Gln	Asp	Lys	Ile	Asp	Thr	Gln	Arg	Arg	Thr	Tyr	Glu	Leu	Asn	Thr	275	280	285	
Leu	Ser	Ala	Gln	Gln	Lys	Gln	Asn	Ile	Gly	Arg	Ala	Thr	Met	Glu	Thr	290	295	300	
Ser	Ala	Val	Ala	Gly	Asn	Ile	Ser	Thr	Ser	Gly	Gly	Arg	Tyr	Ala	Ser	305	310	315	320
Ala	Leu	Glu	Glu	Glu	Gln	Leu	Ile	Ser	Gln	Ala	Ser	Ser	Lys	Gln		325	330	335	

Ala Glu Glu Ala Ser Gln Val Ser Lys Glu Ala Ser Gln Ala Thr Asn  
340 345 350

Gln Leu Ile Gln Lys Leu Leu Asn Ile Ile Asp Ser Ile Asn Gln Ser  
355 360 365

Lys Asn Ser Ala Ala Ser Gln Ile Ala Gly Asn Ile Arg Ala  
370 375 380

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<212> DNA

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<221> misc\_feature

<222> (1)..(4)

<223> NdeI restriction site

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gaga

4

<210> 4

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<222> (1)..(29)

<223> PCR Primer

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gagacatatg ttatcagagc aggttcagc

29

<210> 5

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<221> misc\_feature

<222> (1)..(30)

<223> PCR Primer

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gagaggatcc ttaagctcga atgttaccag

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<210> 6

<211> 27

<212> DNA

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<222> (1)..(27)

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gagacatatg ttgcaaaagc aatttgc

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<210> 7

<211> 32

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<221> misc\_feature

<222> (1)..(32)

<223> PCR Primer

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<210> 8

<211> 29

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<213> Artificial

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<221> misc\_feature

<222> (1)..(29)

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<210> 9

<211> 32

<212> DNA

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<221> misc\_feature

<222> (1)..(32)

<223> PCR Primer

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gagaggatcc ttaggtgtca attttatacct gc

32

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<400> 10  
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22

<210> 11  
<211> 29  
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<223> PCR Primer

<400> 11  
gagactcgag atgcgttttt ttggcaccg

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<223> PCR Primer

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<223> PCR Primer

<400> 13

gagaggatcc ttaagctcga atgttaccag

30

<210> 14  
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<223> PCR Primer

<400> 14  
gagacatatg ttgcaaaagc aatttgc

27

<210> 15  
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<223> PCR Primer

<400> 15  
gagactcgag taactttaaa agttgatcat c

31

<210> 16  
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<222> (1)..(28)  
<223> PCR Primer

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gagactcgag cttgccactg ctcaatct

28

<210> 17  
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<220>  
<221> misc\_feature  
<222> (1)..(30)  
<223> PCR Primer

<400> 17

gagaggatcc ttaagctcga atggtaccag

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## SEQUENCE LISTING

<110> University of Kansas Center for Research  
Walter Reed Army Institute for Research

<120> METHODS FOR THE PRODUCTION OF PURIFIED INVASIN PROTEIN AND USE THEREOF

<130> UOK 5320.1

<150> PCT/US99/24931

<151> 1999-10-21

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 409

<212> PRT

<213> Salmonella typhimurium

<400> 1

Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn Asn  
1 5 10 15

His Ser Val Glu Asn Ser Ser Gln Thr Ala Ser Gln Ser Val Ser Ala  
20 25 30

Lys Asp Ile Leu Asn Ser Ile Gly Ile Ser Ser Ser Lys Val Ser Asp  
35 40 45

Leu Gly Leu Ser Pro Thr Leu Ser Ala Pro Ala Pro Gly Val Leu Thr  
50 55 60

Gln Thr Pro Gly Thr Ile Thr Ser Ser Leu Lys Ala Ser Ile Gln Asn  
65 70 75 80

Thr Asp Met Asn Gln Asp Leu Asn Ala Leu Ala Asn Asn Val Thr Thr  
85 90 95

Lys Ala Asn Glu Val Val Gln Thr Gln Leu Arg Glu Gln Gln Ala Glu  
100 105 110

Val Gly Lys Phe Phe Asp Ile Ser Gly Met Ser Ser Ser Ala Val Ala  
115 120 125

Leu Leu Ala Ala Ala Asn Thr Leu Met Leu Thr Leu Asn Gln Ala Asp  
130 135 140

Ser Lys Leu Ser Gly Lys Leu Ser Leu Val Ser Phe Asp Ala Ala Lys  
145 150 155 160

Thr Thr Ala Ser Ser Met Met Arg Glu Gly Met Asn Ala Leu Ser Gly  
165 170 175

Ser Ile Ser Gln Ser Ala Leu Gln Leu Gly Ile Thr Gly Val Gly Ala

180

185

190

Lys Leu Glu Tyr Lys Gly Leu Gln Asn Glu Arg Gly Ala Leu Lys His  
195 200 205

Asn Ala Ala Lys Ile Asp Lys Leu Thr Thr Glu Ser His Ser Ile Lys  
210 215 220

Asn Val Leu Asn Gly Gln Asn Ser Val Lys Leu Gly Ala Glu Gly Val  
225 230 235 240

Asp Ser Leu Lys Ser Leu Asn Ile Arg Lys Pro Val Pro Met Arg Arg  
245 250 255

Lys Ile Leu Met Met Arg Arg Leu Asn Leu Met Pro Glu Pro Ala Pro  
260 265 270

Arg Lys Val Trp Val Leu Lys Thr Val Ile Asn Lys Val Ser Leu Asn  
275 280 285

Ile Tyr Ile Leu Ser Lys Arg Leu Glu Ser Val Glu Ser Asp Ile Arg  
290 295 300

Leu Glu Gln Asn Tyr Met Asp Ile Thr Arg Ile Asp Ser Ala Gln Asp  
305 310 315 320

Ala Asp Asp Gly Arg Ser Asp Tyr Glu Glu Leu Gly His Gly Arg Trp  
325 330 335

Tyr Cys Arg Gly Val Arg Ala Val Arg Arg Tyr Ser Gly Asn Val Ser  
340 345 350

Glu Gln Gln Ile Ser Gln Val Asn Asn Arg Val Ala Ser Thr Ala Ser  
355 360 365

Asp Glu Ala Arg Glu Ser Ser Arg Lys Ser Thr Ser Leu Ile Gln Glu  
370 375 380

Met Leu Lys Thr Met Glu Ser Ile Asn Gln Ser Lys Ala Ser Ala Leu  
385 390 395 400

Ala Ala Ile Ala Gly Asn Ile Arg Ala  
405

<210> 2

<211> 382

<212> PRT

<213> *Shigella flexneri*

<400> 2

Met Leu Gln Lys Gln Phe Cys Asn Lys Leu Leu Leu Asp Thr Asn Lys  
1 5 10 15

Glu Asn Val Met Glu Ile Gln Asn Thr Lys Pro Thr Gln Thr Leu Tyr  
20 25 30

Thr	Asp	Ile	Ser	Thr	Lys	Gln	Thr	Gln	Ser	Ser	Ser	Glu	Thr	Gln	Lys	35	40	45	
Ser	Gln	Asn	Tyr	Gln	Gln	Ile	Ala	Ala	His	Ile	Pro	Leu	Asn	Val	Gly	50	55	60	
Lys	Asn	Pro	Val	Leu	Thr	Thr	Thr	Leu	Asn	Asp	Asp	Gln	Leu	Leu	Lys	65	70	75	80
Leu	Ser	Glu	Gln	Val	Gln	His	Asp	Ser	Glu	Ile	Ile	Ala	Arg	Leu	Thr	85	90	95	
Asp	Lys	Lys	Met	Lys	Asp	Leu	Ser	Glu	Met	Ser	His	Thr	Leu	Thr	Pro	100	105	110	
Glu	Asn	Thr	Leu	Asp	Ile	Ser	Ser	Leu	Ser	Ser	Asn	Ala	Val	Ser	Leu	115	120	125	
Ile	Ile	Ser	Val	Ala	Val	Leu	Leu	Ser	Ala	Leu	Arg	Thr	Ala	Glu	Thr	130	135	140	
Lys	Leu	Gly	Ser	Gln	Leu	Ser	Leu	Ile	Ala	Phe	Asp	Ala	Thr	Lys	Ser	145	150	155	160
Ala	Ala	Glu	Asn	Ile	Val	Arg	Gln	Gly	Leu	Ala	Ala	Leu	Ser	Ser	Ser	165	170	175	
Ile	Thr	Gly	Ala	Val	Thr	Gln	Val	Gly	Ile	Thr	Gly	Ile	Gly	Ala	Lys	180	185	190	
Lys	Thr	His	Ser	Gly	Ile	Ser	Asp	Gln	Lys	Gly	Ala	Leu	Arg	Lys	Asn	195	200	205	
Leu	Ala	Thr	Ala	Gln	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Gly	Ser	Lys	Leu	210	215	220	
Gly	Leu	Asn	Lys	Gln	Ile	Asp	Thr	Asn	Ile	Thr	Ser	Pro	Gln	Thr	Asn	225	230	235	240
Ser	Ser	Thr	Lys	Phe	Leu	Gly	Lys	Asn	Lys	Leu	Ala	Pro	Asp	Asn	Ile	245	250	255	
Ser	Leu	Ser	Thr	Glu	His	Lys	Thr	Ser	Leu	Ser	Ser	Pro	Asp	Ile	Ser	260	265	270	
Leu	Gln	Asp	Lys	Ile	Asp	Thr	Gln	Arg	Arg	Thr	Tyr	Glu	Leu	Asn	Thr	275	280	285	
Leu	Ser	Ala	Gln	Gln	Lys	Gln	Asn	Ile	Gly	Arg	Ala	Thr	Met	Glu	Thr	290	295	300	
Ser	Ala	Val	Ala	Gly	Asn	Ile	Ser	Thr	Ser	Gly	Gly	Arg	Tyr	Ala	Ser	305	310	315	320
Ala	Leu	Glu	Glu	Glu	Gln	Leu	Ile	Ser	Gln	Ala	Ser	Ser	Lys	Gln		325	330	335	

Ala Glu Glu Ala Ser Gln Val Ser Lys Glu Ala Ser Gln Ala Thr Asn  
340 345 350

Gln Leu Ile Gln Lys Leu Leu Asn Ile Ile Asp Ser Ile Asn Gln Ser  
355 360 365

Lys Asn Ser Ala Ala Ser Gln Ile Ala Gly Asn Ile Arg Ala  
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